

Species composition and abundance of the shallow water fish community of Kongsfjorden, Svalbard

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Abstract Projections show that climate change will lead to structural change in Arctic ecosystems. Studies project the extinction of local species and intense species invasion to the Arctic Ocean. A lack of basic biological data about the Arctic shallow water fish community will make it hard to assess whether these communities will change or not. Baseline studies in combination with future reassessments are needed to establish a basic knowledge about the change of these communities. This study provides a quantitative first time description of the shallow water fish community of Kongsfjorden, Svalbard. The fish assemblage in the depth range from 3 to 12 m was determined with respect to abundance and species composition. Among a total sample size of 2804 specimens, the presence of 12 fish species and one family (Liparidae) was detected. *Myoxocephalus scorpius* (shorthorn sculpin) (74.9 %), *Gadus morhua* (Atlantic cod) (17.2 %), and *Gymnocanthus tricuspis* (Arctic staghorn sculpin) (3.8 %) were identified as the most abundant species across all sampling sites. A significant relationship between algal coverage and fish abundance was detected. Furthermore, we demonstrated a fjord inward increase in biodiversity along the south shore that might be correlated with a change in hydrographic regime.

Keywords Demersal · Sublittoral · Coastal habitats · Algal belts · Species diversity

Introduction

It is known that climate change can impact the marine biodiversity through changes in species distribution. Existing projections for marine fish and invertebrates show local species extinctions and intense species invasions into the Arctic Ocean (Cheung et al. 2009). Consequently, Arctic fishes might not just experience a change of hydrographic regime, but may also face new ecological interactions (Fossheim et al. 2015). Due to a lack of basic ecological data about Arctic fishes, the consequence for ecosystem structure and function is unclear (Christiansen et al. 2014). A possible scenario is the retreat of Arctic shelf fish species northwards towards the polar basin and a borealisation of the southern communities (Fossheim et al. 2015). However, a thorough quantitative assessment of Arctic fish communities, to which future investigations can be compared, has hitherto been lacking especially for Arctic shallow water habitats. This study aims to provide this description for the shallow water habitat of Kongsfjorden.

Kongsfjorden on the west coast of Spitsbergen (Fig. 1) has been the focus of ecological research in the Arctic for several decades. Geographically, Kongsfjorden at 79°N is classified as Arctic; however, it is in fact significantly influenced not only by Arctic but also by Atlantic water masses from the Fram Strait (Hop et al. 2002). The 20 km long fjord opens to a shelf system in a westerly direction without a sill and shares this outlet with the more northern Krossfjorden (Cottier et al. 2005). Additionally, an underwater canyon runs from the outlet across the shelf to the

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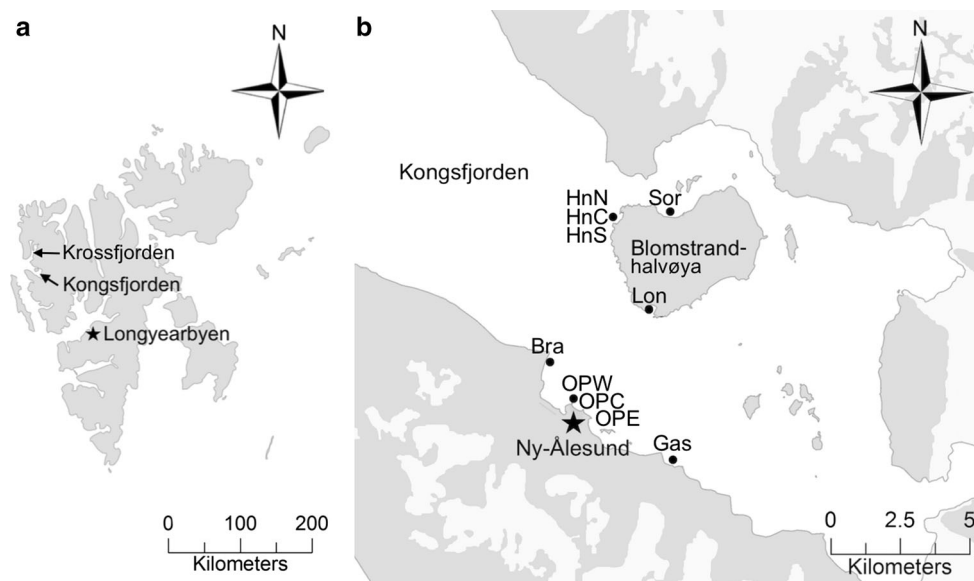


Fig. 1 **a** Map of the Svalbard archipelago with its main settlement Longyearbyen and the site of study, Kongsfjorden. **b** Map of Kongsfjorden with its settlement Ny-Ålesund and the island Blomstrandhalvøya. Light areas on land indicate glacier surfaces. The sampling sites are marked with abbreviations: Sor—Sørvågen, HnN—Hansneset North, HnC—Hansneset Central, HnS—Hansneset

South, Lon—London, Bra—Brandal, OPW—Old Pier West, OPC—Old Pier Central, OPE—Old Pier East, Gas—Gåsebu. The three sites at Hansneset and Old Pier were spaced approximately 100 m from each other. The map data were provided by the Norwegian Polar Institute

continental edge, establishing a connection to the deeper water masses off the shelf that belong to the West Spitsbergen Current. Complex mixing processes between the Arctic shelf water masses, the Atlantic deep water masses, and the highly seasonal fresh water run-off from the inner part of the fjord result in steep environmental gradients from the inner parts of the fjord up to its mouth (Svendsen et al. 2002). Willis et al. (2006) suggest a general counter-clockwise circulation pattern in Kongsfjorden for the transport and the mixing of those water masses with an influx of water along the south shore and an efflux along the north shore. The resulting hydrographic gradients and their short- and long-term changes in intensity have the potential to directly influence the pelagic and benthic realms of the fjord. Thereby, the local food web is influenced on a spatial and temporal scale (Stempniewicz et al. 2007).

The complex environmental interactions within the fjord result in a mixed species composition that includes Atlantic and Arctic species in close association. The study of this dynamic habitat and its ecological processes is potentially valuable to enhance the knowledge about the potential influence of hydrographic regime shifts on other Arctic ecosystems. The general differences and characteristics of each ecosystem will have to be carefully reviewed for such comparison, but in the context of a predicted rise of 3.7 °C in mean air temperature in the Arctic over the next 50 years (ACIA 2004; Wong et al. 2014), Arctic marine

ecosystems might face similar long-term changes in their hydrographic regimes, e.g., a rise of sea surface temperature and a general decrease of ice cover potentially directly affecting the marine habitat and its fauna. In the outer part of Kongsfjorden, a close relationship between short-term hydrographical regime changes and the zooplankton abundance has already been shown by Willis et al. (2006). In contrast, Renaud et al. (2011) used stable isotope ratios to demonstrate relative little variability in food web structure of Kongsfjorden over the temporal and spatial scale of their study. In turn, Voronkov et al. (2013) showed for hard bottom zoobenthos a general decrease in species richness, frequency of occurrence, mean abundance, and biomass towards the tidal glaciers in inner Kongsfjorden. Hop et al. (2002) highlight the need to better understand the temporal and spatial dynamics of the secondary and tertiary consumers including zooplankton, crustaceans, fishes, birds, and mammals, as well as their interaction with the local hydrographical regime.

Previous fish community assessments in Kongsfjorden have been performed by trawling in the deeper parts of the fjord or by diving observations in the shallow areas (Hop, pers. comm.). Recent studies describe a total of about 30 Arctic, sub-Arctic, and boreal fish species for the entire fjord system. Typical species with an Arctic and sub-Arctic distribution are *Boreogadus saida* (polar cod), *Eumicrotremus derjungini* (leatherfin lumpsucker), *G. tricuspsis* (Arctic staghorn sculpin), *Lycodes reticulatus* (Arctic

eelpout), *Mallotus villosus* (capelin), *Sebastes mentella* (deepwater redfish), and *Somniosus microcephalus* (Greenland shark). Furthermore, generalist species of the North Atlantic can be found. These are *G. morhua* (Atlantic cod), *M. scorpius* (shorthorn sculpin), *Anarhichas lupus* (Atlantic wolffish), *Leptoclinus maculatus* (daubed shanny), *Hippoglossoides platessoides* (long rough dab), *Leptagonus decagonus* (Atlantic poacher), and the family of Liparidae (snailfishes) (Hop et al. 2002; Renaud et al. 2011). The shallow water habitat of Kongsfjorden has been described by SCUBA surveys as rich in macroalgal belts (Hop et al. 2012). Bartsch et al. (2016) showed for 2012 and 2013 that the maximum density of these kelp belts was found at a depth of 2.5 m, with decreasing densities down to the maximum depth of the study at 15 m. Jørgensen and Gulliksen (2001) described the seabed in depths between 16 and 30 m as highly structured and complex benthic habitat with a mixture of rocky bottom, ice-rafted pebbles and stones. Voronkov et al. (2013) report that the structural complexity of the seafloor is increased by crustose coralline algae, shell hash of molluscs, and barnacles. The maximum abundance and diversity of hard bottom fauna are described by Voronkov et al. (2013) for the depth range of 5–10 m in 1996–1998. The structure rich seafloor has the potential to represent an important habitat for fishes. Especially, the macroalgal belts provide additional structural protection from waves as well as currents, and the infauna is a potential food source (Lippert et al. 2001). The shallow water habitats are commonly considered to be areas of aggregation for the resident fish community due to their function as spawning and nursery grounds (Werner 1977; Werner et al. 1983; Keast 1985; Pierce et al. 1994; Fischer and Eckmann 1997a, b). By feeding in the macroalgal belts, the fish community acts as a secondary producer in the local food web making them potentially important for energy and matter flux. Recent studies of Bartsch et al. (2016) and Paar et al. (2016) show significant changes in the structure of the macroalgal belt at Hansneset and also its macrozoobenthos community between 1996 and 1998 and 2012–2014. In comparison with previous studies, these changes might be caused by an increase of ice-free days over the last decade and a decrease in ice scouring, but the lack of quantitative baseline data for the shallow water fish community in Kongsfjorden makes it impossible to detect potential changes in relation to shifts in habitats and prey. Potential changes in abundance and species composition of the fish community will have direct effects on other compartments of the food web. To close this gap for future studies, the principal goal of this study is to provide the first quantitative overview of the fish species richness and abundance, as well as spatial distribution patterns of demersal fish in the shallow waters of Kongsfjorden and how it relates to habitat complexity. The data

presented in this study were sampled in parallel to the field work published in Bartsch et al. (2016) and Paar et al. (2016) in 2012 and 2013 including the sampling site Hansneset and further sites in the central part of Kongsfjorden. While this study provides baseline data of the fish community, further collaborative publications will cover the role of the fish community in the food web and its seasonal dynamics.

Materials and methods

The study area was the central part of Kongsfjorden, Svalbard (Fig. 1). In 2012, we sampled in week 24–28 and 36–39. In 2013, sampling was performed from week 23 to 30 and 35–40. In 2012, only one sampling site at the southern shoreline (Old Pier Central; Fig. 1b) and one at the shoreline of the island Blomstrandhalvøya (Hansneset South; Fig. 1b) were chosen, because it was unclear how feasible a more intense sampling program would be. The two sampling sites were chosen for coherence with linked projects. The site Hansneset was used for macroalgal research (Wiencke et al. 2004; Fredriksen et al. 2014; Bartsch et al. 2016; Paar et al. 2016), and at the site Old Pier Central, the Kongsfjorden Underwater Observatory was deployed. Additionally, we expected that the counter-clockwise water mass circulation in Kongsfjorden (Willis et al. 2006) might influence the fish community on the opposite shorelines of Kongsfjorden.

With logistical support from the research management company KingsBay and the AWIPEV research station in 2012, we extended the sampling scheme in 2013 to six sampling areas, consisting of three areas at the northern shoreline around Blomstrandhalvøya (Sørvågen, Hansneset and London; Fig. 1b) and three areas at the southern shoreline (Brandal, Old Pier and Gåsebu; Fig. 1b). Starting with week 26 in 2013 one sampling area at each shoreline (Hansneset and Old Pier) was sampled at three subsites (Hansneset North, Hansneset Central and Hansneset South; Old Pier West, Old Pier Central and Old Pier East). The subsites were 50–75 m apart from each other. The triplicate sampling design at the respective middle sites of each shoreline was performed to provide an estimate of the variability within a sampling area. From the beginning of the study up to week 36 of 2012, sampling was performed at each of the two sites using one fyke net [diameter 40 cm, length 90 cm, mesh size 12 mm (bar mesh)], deployed in about 3 m water depth with its mouth set perpendicular to the shoreline and one trammel net (inner/outer mesh size 1/15 cm, length 20 m, height 2 m) deployed from about 5 to 12 m water depth. The distance to the shoreline depended on the slope of the seafloor, and ranged from 5 to 50 m.

During an equipment test in week 35 of 2012, we monitored an interaction of young seals with the trammel nets, indicating potential for entanglement. In response, we decided to replace all trammel nets by sets of three fyke nets per sampling site. One fyke net [diameter 40 cm, length 90 cm, mesh size 12 mm (bar mesh)], was deployed in about 3 m water depth and a second one of the same type in 12 m water depth. Additionally, a double fyke net [diameter 60 cm, length 110 cm, mesh size 12 mm (bar mesh)], connected by a 10 m long, 80 cm high steering net (18 mm bar mesh) was laid out between 5 and 8 m water depth. All nets were laid out in line with their mouths set perpendicular to the shoreline. We also started to place bait (fish muscle tissue) in the fyke nets at 3 and 12 m water depth to increase the fish catches in the solitaire fyke nets. The plan was not to compare between nets with and without bait, but only to do analysis between identical sets of nets at different sampling sites. The sampling design was maintained from this point on for all further samplings in 2012 and in 2013.

The net exposure time was normally 24 h. However, logistic and weather conditions occasionally delayed net recovery to exposure times of up to 96 h. To calculate the effects of a delayed net recovery on the mean catch efficiency, we back-calculated all catches to 24 h exposure time and compared the number of fishes caught per 24 h, per net (CPUE) of the catches with 24 h \pm 3 h exposure time ($N = 566$), 72 \pm 3 h exposure time ($N = 276$) and 96 \pm 3 h exposure time ($N = 130$). Because we had no simultaneous catches for 24, 72 and 96 h at one site and one timepoint to make a real experimental comparison of the effects of exposure time on the CPUE, we included all catches in the analysis to avoid hidden structural site or time effects, which we could not predict. We used three Bonferroni-corrected unpaired two-group Wilcoxon and Mann–Whitney Tests (Wilcoxon 1945; Mann and Whitney 1947), to compare all CPUE values of the three classes with each other. The tests revealed no significant difference between the three exposure time scenarios (24 vs. 72 h, $W = 78,512$, $p = 0.90$; 24 vs. 96 h, $W = 33,947.5$, $p = 0.16$; 72 vs. 96 h, $W = 17,086$, $p = 0.44$). All sampled fishes were identified to species level by morphological characteristics (Able 1990; Węśławski et al. 1990; Muus and Nielsen 1999; Hayward and Ryland 2005), except for fishes of the family Liparidae due to the potential for errors.

Standard length (SL) of all fishes was determined to the nearest 0.5 cm, and specimen was weighed with a precision of 1 g wet weight. For analysing species occurrence over all sampling sites, as well as species-specific size distribution, we used all fishes sampled in 2012 and 2013. Note that the length frequency distribution is only presented for the most abundant species, due to the sample

size. For all site comparative analyses, however, we only used the data from week 26 to 40 of 2013, because during this time-period, all sites and subsites were sampled in parallel with an equivalent total fishing effort. Based on the absolute number of fishes caught at the sampling sites in this period, ecological metrics were calculated. Species richness (S) (Colwell 2009) was calculated as the total number of species per site. However, Colwell stated that a comparison of S values among different sites might be biased by significant differences in total abundance among these sites. Because of differences in the sample sizes between our sampling sites, we additionally calculated the rarefied species richness (Raup 1975). It is based on a random subsampling of the total samples to of every site. By this method, a standardised species richness for a sample size of $N = 100$ per site was calculated. Furthermore, the Shannon-Wiener diversity (H') (Shannon 1948) and the associated species evenness ($J = H'/\ln(S)$) (Pielou 1966) were determined to evaluate species richness values independent of the total fish abundances at the different sites. These calculations were performed by the software Diversity (Version 1.6.2; Holland 2010).

An Ad Hoc opportunity allowed us to assess the structure of the seafloor in the six sampling areas from 15 July 2013 to 27 July 2013 by SCUBA diving and visual census. This made it possible to gather information about the habitat complexity of our fishing sites. All SCUBA assessments were carried out according to the German diving standard for scientific diving written in BGR/GUV-R 2112 (DGUV 2011). For these assessments, we used a 55 m long line on a diving reel. It was deployed in parallel to the sets of fyke nets. It started in water of 3 m depth down to the 12 m bathymetric contour. Depending on the slope of the coastline, the line did not extent to a water depth of 12 m, but was never shallower than the lower end of the double fyke net (minimum 8 m). The line had marks every meter and special marks every 10 m to give the observer distance information. A scientific diver followed the line with a head-mounted video camera, keeping a vertical distance of 1.5 m. The seafloor was thereby captured on video for a distance of about 1 m on both sides of the transect line. The videos were analysed in 5 m steps to assess (a) the percentage coverage by algae on an ordinal scale using the classes <25 , 25–50, 50–75 and >75 %; (b) the sediment structure using the nominal classifications of sand, gravel, rock, and unidentified. All video analyses were performed repeatedly and independently by five divers. The values of the five divers were integrated by calculation of the modal value to a single value per 1×5 m segment.

To compare the abundance of fish at the different fishing sites, a CPUE value was calculated per site and sampling week. It is the average number of fish caught in one fyke

net in 24 h. Because homogeneity of variance and normal distribution were not given, we chose to use the nonparametric Kruskal–Wallis rank sum test (Kruskal and Wallis 1952) for further analysis. First, we grouped the CPUE values according to their sampling sites, and analysed possible differences. Moreover, we grouped the CPUE values based on the location of the sampling site (Blomstrandhalvøya or south shore) and the modal value determined for the algal coverage per site. We repeated this analysis for species diversity, i.e., we determined the total number of species we caught per site and week. We grouped them for the four different analyses according to sampling site, location, and algal coverage. All tests and transformations were performed in R (R Core Team 2015). When significant differences were detected by the Kruskal–Wallis test, we used the Nemenyi tests for multiple comparisons of rank sums for post hoc analysis (Nemenyi 1963). We chose this test as it compensates for family-wise error with Chi squared approximation. For these operations, the R-Package PMCMR (Pohlert 2015) was used. Both analyses were performed with a significance level of 5 %.

To further analyse the inter-site differences in species abundance in more detail, we created a Bray–Curtis resemblance matrix based on the total number of each fish species per site, divided by the total fishing effort per site. The data were square-root transformed to reduce the effect of the highly abundant species. The resemblance matrix was used to create a two-dimensional non-metric multidimensional scaling (MDS) plot (Clarke 1993). Additionally, similarities were analysed by hierarchical cluster analysis using group means (Byrne and Uprichard 2012). These operations were performed with the software Primer 6 (Clarke and Gorley 2006). Bar charts and their metrics were calculated using R (R Core Team 2015) with the additional packages gplots (Warnes et al. 2015), lawstat (Hui et al. 2008), and reshape (Wickham 2007).

Results

Integrated over all fishing campaigns in 2012 and 2013, a total of 2804 fish and 12 species (including the family Liparidae, which counted as a single group) were caught (Table 1). All species caught by the trammel nets in 2012 were also caught with the fyke nets. The only exception represents the two specimen of *Amblyraja radiata* (thorny skate), which were both caught in trammel nets. The three most common fish species in the catches were *M. scorpius*, with a total contribution of 74.9 %, *G. morhua* with a 17.2 % contribution, and *G. tricuspis* with a 3.8 % contribution. Fish of the family Liparidae represented a total

contribution of 2.3 %. All other species including *Anarhichas lupus*, *Melanogrammus aeglefinus* (haddock), *B. saida*, *Pollachius virens* (saithe), *Lumpenus lampraetiformis* (snake blenny), *A. radiata*, *Clupea harengus* (Atlantic herring), and *Cyclopterus lumpus* (lumpfish) were caught in much lower abundances, with contributions below 1 % per species (Table 1).

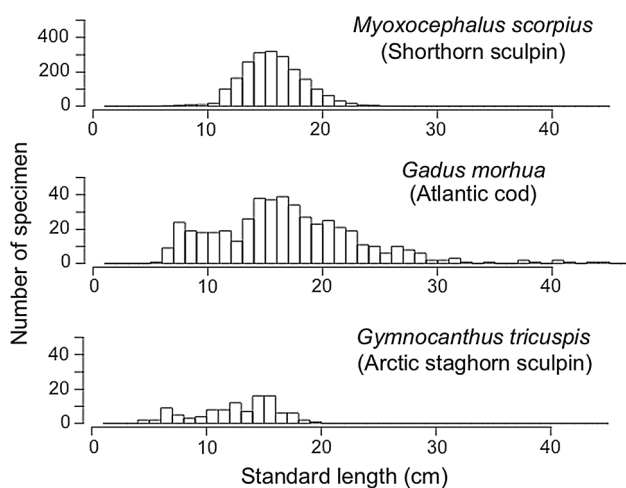
The modal value for standard length was 15.0 cm for *M. scorpius*, 15.0 cm for *G. morhua*, 14.5 cm for *G. tricuspis*, and 10.0 cm for Liparidae. (Table 1). Further analysis of the species-specific length data (Fig. 2) revealed a comparatively uniform length–frequency distribution in *M. scorpius*, with a maximum near its arithmetic mean (1st quartile 14 cm, median 16 cm, 3rd Quartile 17.5 cm). *G. morhua* showed a much wider and almost bimodal length–frequency distribution with a first maximum at 7 cm and a second maximum between 15 and 17 cm. A similar bimodal length–frequency distribution was also observed for *G. tricuspis* with a first maximum at 6 cm and a second maximum between 15 and 16 cm.

Based on the dataset of 2013, we compared the different sampling sites in Kongsfjorden (Table 2). The CPUE (average number of fish per net in 24 h) of the sites around Blomstrandhalvøya was 1.11 (SD = 0.64), while the sites at the south shore showed a value of 0.78 (SD = 0.54) (Fig. 3). A Kruskal–Wallis test showed a significant difference in CPUE between the two coastlines (χ^2 (1, $N = 110$) = 11.47, $p < 0.01$). The average number of species counted per sampling week was 2.76 (SD = 0.77) for the sampling sites at Blomstrandhalvøya, and 2.25 (SD = 0.77) for the sampling sites at the south shore. The Kruskal–Wallis rank sum test reports the two groups as significantly different (χ^2 (1, $N = 110$) = 10.691, $p < 0.01$). A site wise comparison of weekly CPUE and number of species could show no statistical significant differences (Fig. 3).

The underwater mapping of the six sampling sites showed distinct differences with respect to algal coverage and sediment structure (Table 3). The grouping of CPUE according to the modal value of algal coverage at the sampling sites shows also differences. The highest average CPUE was detected at the sites with the lowest algal coverage (1.1, SD = 0.94), the second highest at the sites of densest algal coverage (0.96, SD = 0.49). Statistical analysis reveals a significant difference between the sites of 50–75 % algal coverage and 75–100 % coverage (χ^2 (9, $N = 66$) = 12.483, $p < 0.01$). The grouping of the total number of species per week and site according to algal coverage showed the highest species diversity at the site with the highest (75–100 %) and the lowest (25–50 %) algal coverage. The site with the intermediate (50–75 %) algal coverage showed the lowest average number of

Table 1 Species list of all catches in 2012 and 2013. The total catch is presented for the two fishing set-ups used in this study. The percentage is calculated by the sum of all specimens caught. The minimum, maximum, and modal value of standard length is presented

Species name	Total catch per net set-up		Total (%)	Standard length (cm)	
	Trammel nets, fyke nets 10 June 2012–09 September 2012	Double fyke nets, fyke nets w. bait 10 September 2012–06 October 2013		Range	Modal value
<i>Myoxocephalus scorpius</i> Linnaeus, 1758	557	1543	74.89	5.0–26.5	15.0
<i>Gadus morhua</i> Linnaeus, 1758	63	420	17.23	5.5–82.0	15.0
<i>Gymnocanthus. tricuspis</i> Reinhardt, 1830	22	85	3.82	4.5–20	14.5
Liparidae	4	59	2.25	6.0–19	10.0
<i>Anarhichas lupus</i> Linnaeus, 1758	3	10	0.46	28.0–61.5	42.0
<i>Melanogrammus aeglefinus</i> Linnaeus, 1758	11	1	0.43	6.0–19.0	17.5
<i>Boreogadus saida</i> Lepechin, 1774	0	10	0.36	21.0–30.0	25
<i>Pollachius virens</i> Linnaeus, 1758	0	6	0.21	6.0–16.5	NA
<i>Lumpenus lampretaeformis</i> Wallbaum, 1792	1	4	0.18	24.0–41.0	40.5
<i>Amblyraja radiata</i> Donovan, 1808	2	0	0.07	54.0–54.0	54.0
<i>Clupea harengus</i> Linnaeus, 1758	0	2	0.07	19.0–19.0	NA
<i>Cyclopterus lumpus</i> Linnaeus, 1758	0	1	0.04	20.0–20.0	20.0

**Fig. 2** Cumulative standard length distributions of the three most abundant fish species, *M. scorpius*, *G. morhua* and *G. tricuspis*

species. Statistical analysis showed a distinct difference between 50–75 % algal coverage and 75–100 % coverage (χ^2 (2, $N = 66$) = 11.576, $p < 0.01$).

The total number of species per site varied between four and seven for the whole sampling period (Table 2). The highest values of species richness (seven species) were found at the sites Hansneset Central, Hansneset South, and London along the shoreline of Blomstrandhalvøya. The sites with the lowest total number of species (four species) were Old Pier East (south shore) and Hansneset North (Blomstrandhalvøya) (Table 2). The calculation of the rarefied species richness for a unified sampling size of $N = 100$ per site showed similar results with the highest values at the sites Hansneset Central (6.3) and London (6.2) and the lowest values at the sites Old Pier East (3.5) and Old Pier West (4.0) (Table 2). The calculated values for Shannon's H' integrate information about species richness and abundance. An apparent gradient was observed along the southern shoreline with the lowest H' value of 0.51 at the site Brandal and the highest value of 1.05 at the innermost sampling site, Gåsebu (Table 2). At the shoreline of Blomstrandhalvøya, H' values between 0.75 and 1.01 were observed with four of five stations having values between 0.95 and 1.01. A comparable west–

Table 2 Species composition and abundance per sampling site. Additionally ecological indices for each sampling site are presented

	Sampling site									
	Brandal	Old Pier West	Old Pier Central	Old Pier East	Gåsebu	Sørvågen	Hansneset North	Hansneset Central	Hansneset South	London
Species composition (%)										
<i>Myoxocephalus scorpius</i>	88.46	75.73	74.19	80.09	60.95	67.69	72.88	60.74	64.19	68.46
Linnaeus, 1758										
<i>Gadus morhua</i>	6.15	17.48	17.34	15.17	21.30	20.77	20.90	32.59	25.33	18.12
Linnaeus, 1758										
<i>G. tricuspidis Reinhard, 1830</i>	2.31	5.83	4.44	4.27	14.79	5.38	0.56	0.74	0.44	6.04
Liparidae	1.54	0.49	2.42	0.00	1.78	4.62	5.65	0.74	7.42	4.70
Other	1.54	0.49	1.61	0.47	1.18	1.54	0.00	5.19	2.62	2.68
Fishes per net per day ($n \pm SD$)	0.49 ± 0.17	1.07 ± 0.77	0.79 ± 0.37	0.98 ± 0.69	0.57 ± 0.20	1.62 ± 1.10	1.12 ± 0.44	0.64 ± 0.18	1.18 ± 0.33	0.98 ± 0.34
Species richness	6	5	6	4	6	5	4	7	7	7
Rarefied species richness ($N = 100$)	5.48	3.97	5.15	3.47	5.12	4.95	3.56	6.33	5.38	6.24
Shannon's <i>H</i>	0.51	0.73	0.83	0.62	1.05	0.95	0.75	0.95	0.97	1.01
Pielou's <i>J</i>	0.28	0.46	0.46	0.45	0.58	0.59	0.54	0.49	0.50	0.52

east trend along the southern shoreline was observed for Pielou's *J'* (Pielou 1975), a measure of species evenness. The lowest value was determined for the site Brandal (0.28) and highest value at Gåsebu (0.58). Along the north shore, values ranged between 0.49 at Hansneset Central and 0.59 at Sørvågen (Table 2).

The calculated two-dimensional MDS plot shows a Kruskal stress value of 0.09 (Fig. 4). Ordination of sites occurred in groups according to their general geographical locations from west (left) to east (right). An exception are the sites at Hansneset that cluster on the lower right of the plot. Hierarchical cluster analysis of the Bray–Curtis resemblance matrix was used to add further information to the MDS plot. The overall similarity between all sites was determined to be over 77 %. Using a similarity level of >80 %, two clusters could be discriminated (Fig. 4). One contained Hansneset South, Hansneset North, and Hansneset Central. The second contained all other sites, except the site Brandal, which is not part of any cluster. Two subclusters at a similarity level of >90 % could be identified. The first contained the sites London and Sørvågen, and the second contained Old Pier West and Old Pier Central.

Discussion

This study provides the first systematic field data of the shallow water fish community of this polar ecosystem. According to Hop et al. (2002), such data on the higher trophic levels of shallow water polar ecosystems are completely missing but urgently needed for a basic understanding of the functional responses of Arctic ecosystems to environmental changes like global warming.

Our most striking result is the distinct dominance of the shallow water fish community in Kongsfjorden by the two species *M. scorpius* and *G. morhua*, while other species that were found in previous studies were rare or absent. This is in good agreement with Hop et al. (2002). The apparent lack of *B. saida* in our study, e.g., is most remarkable because previous studies reported high abundances of *B. saida* in the offshore and coastal waters of Kongsfjorden (Haug and Gulliksen 1982). Similarly, we could not detect any *Mallotus villosus*, *Sebastes sp.* (red-fish) or *Hippoglossoides platessoides* (American plaice), which were reported in previous studies (Hop et al. 2002). A key to understand these differences in species occurrence in comparison with previous studies may be the lifestyles of these species. *B. saida* is known to prefer sea ice as habitat for young-of-year (YOY) and older specimen which are often found below sea ice at sub-zero temperatures (Lønne and Gulliksen 1989; Hop and Gjøsæter 2013). The apparent lack of sea ice in Kongsfjorden since the winter of

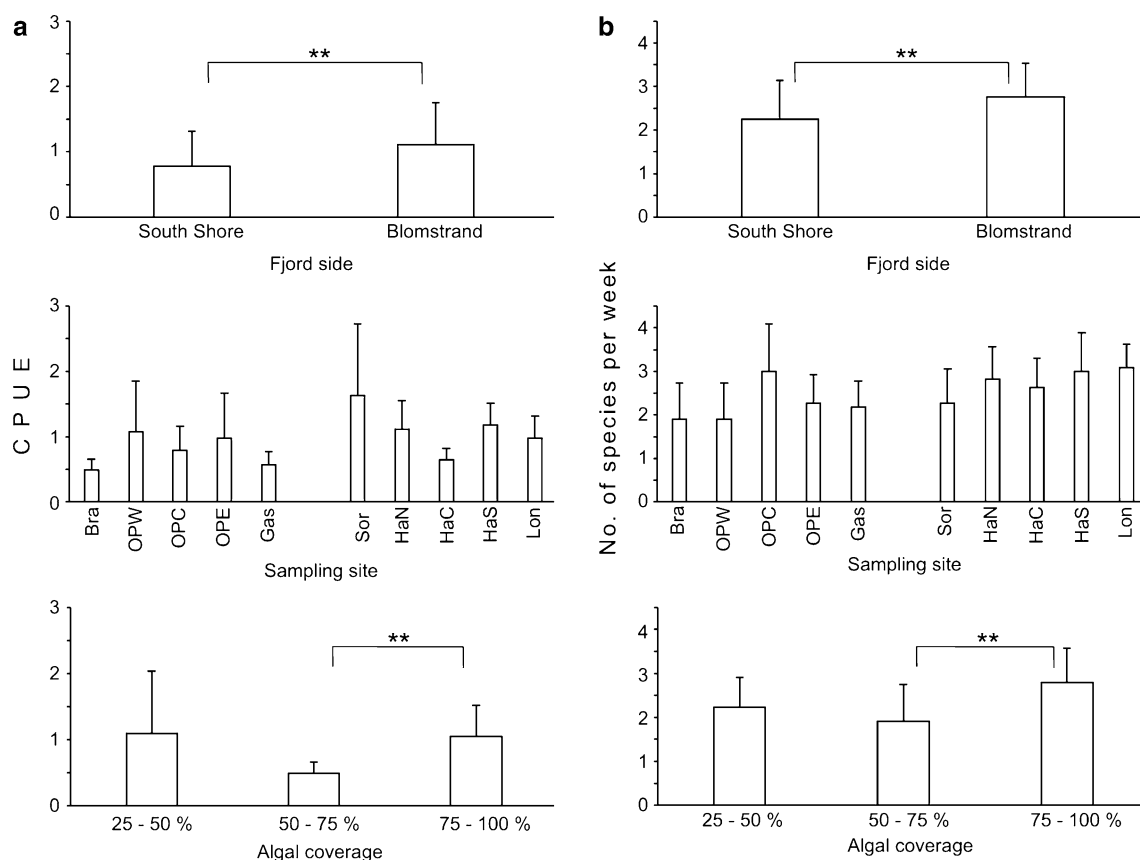


Fig. 3 **a** Number of fish per net SD in 24 h (CPUE) and **b** Total number of species per week. Values are grouped by their geographical location (*upper panel*), their sampling site (*middle panel*) or the modal value of algal coverage at their respective sampling site (*lower panel*)

2005/2006 might therefore be a factor that explains the low abundances of *B. saida* in Kongsfjorden (Cottier et al. 2007). Additionally, Fischer et al. (2016) reports temperatures of 4 to 8 °C from June to September 2014 at 10 m water depth at the Old Pier in Ny-Ålesund. This clearly exceeds the preferred temperature range of *B. saida* and might additionally explain its low abundances. Also Hop et al. (2002) reports that *B. saida* and *M. villosus* could be found in the pelagic realm of the fjord, which was not sampled in this study. For a similar reason, *H. platessoides* might not be represented in this study. This species prefers deeper waters below 90 m, and it is likely that it is therefore not caught in the shallow waters of Kongsfjorden. In contrast, *M. scorpius* is a classic demersal fish species of shallow water habitats (Lamp 1966). Therefore, the dominance of this species in our fyke net catches is not surprising. Also, young specimen of *G. morhua* are well known to seek protection in structural complex shallow water habitats to avoid predators and cannibalisation by larger specimen, explaining the high abundance of this species with younger age classes in the shallow waters.

Another explanation for the dominance of *M. scorpius* and *G. morhua* in our study might be gear selectivity. It is

known that fyke nets are size and species selective (Hubert et al. 2012). Cover-seeking mobile species are reported to be most susceptible to capture by this gear type (Hubert et al. 2012). On the other hand, we minimised size selectivity by small mesh size, and we could not detect a change in species composition with regard to the trammel nets that we used in 2012. The dominance of *M. scorpius* in the shallow areas of Kongsfjorden was also confirmed by continuous diving operations during the last 15 years (Max Schwanitz, pers. com.). Therefore, we doubt that the generally low share of Arctic fishes (<5 %) in our catches in the shallow water system of Kongsfjorden was an artefact.

Parallel to our study Mark (2013) performed trawling catches with RV Heincke in outer Kongsfjorden and also caught *G. morhua* (and the pelagic species *Melanogrammus aeglefinus*) in higher abundances and missed *B. saida*, or *M. villosus* in the catches. Even though this study used a completely different fishing gear, it is most interesting that the species composition was similar to our study with a high dominance of *G. morhua* during 2013. The standard length (SL) of *G. morhua* captured offshore was reported as 5.5–9.5 cm, which was quite below the average length of 15.0 cm in our study. Surveys at the Lofoten in January

Table 3 Algal coverage and sediment structure at the sampling sites from 3 to 12 m water depth. The bottom structure was determined by SCUBA video survey and subsequent video analysis

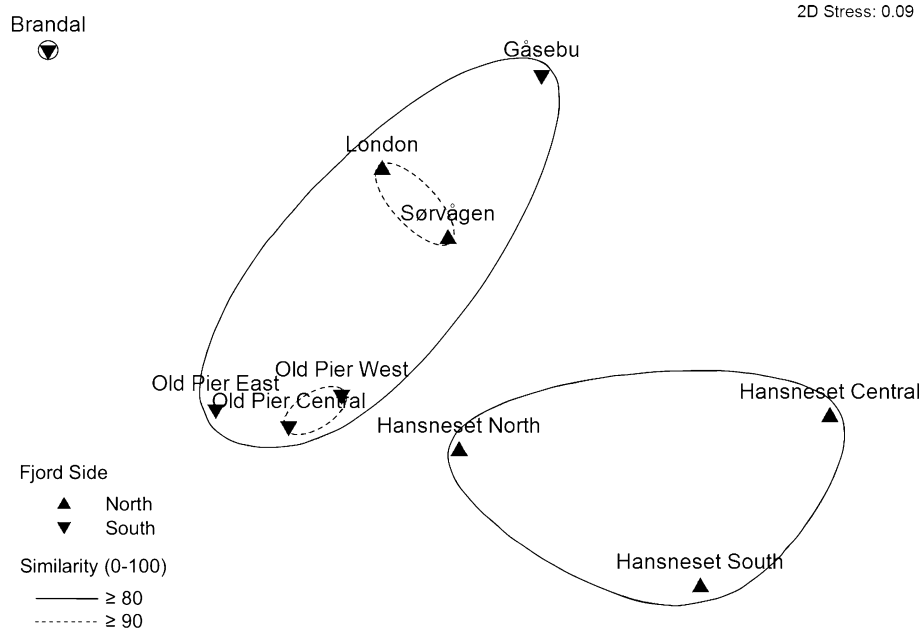
Distance from shore (m)	Brandal	Old Pier East	Gåsebu	Sørvågen	Hansneset South	London
<i>(a) Algal coverage</i>						
5	1	3	2	4	4	2
10	1	4	2	2	4	2
15	2	4	2	4	4	3
20	3	4	2	2	4	3
25	3	4	2	4	4	3
30	2	4	2	3	4	4
35	3	4	1	2	4	4
40	NA	4	2	2	4	4
45	NA	4	2	3	4	4
50	NA	4	2	4	4	4
55	NA	4	2	2	4	4
Modal value	3	4	2	2	4	4
Key		1	2	3	4	
		0–25 %	25–50 %	50–75 %	75–100 %	
<i>(b) Sediment structure</i>						
5	1	1	1	4	4	1
10	1	1	1	4	4	1
15	1	1	1	1	2	1
20	1	1	1	1	2	1
25	1	4	1	1	4	1
30	1	1	1	1	4	1
35	1	1	1	1	4	4
40	NA	1	1	1	4	4
45	NA	2	1	1	4	4
50	NA	2	1	4	4	4
55	NA	1	1	4	4	4
Key	1	1	1	1	4	1
		1	2	3	4	
		Sand	Gravel	Rock	Fully covered	

2002 revealed a mean standard lengths of 12.4 cm at age 1+, 19.9 cm at age 2+ and 31.4 cm at age 3+ (ICES 2005). Assuming a similar growth rate, the majority of Atlantic cod caught in our study belonged to the age classes 1+ and 2+ (Fig. 2) and age-0 fish were almost completely missing. This is interesting with respect to the fact that it is generally assumed that cod in Svalbard belongs to the Arcto-Norwegian cod stock, which is known to spawn along the Norwegian coast from Møre up to East Finnmark (Sarvas and Fevolden 2005; Sundby and Nakken 2008). Assuming that our shallow water specimen and the off-shore YOY specimen from the Heincke cruise belonged to the same stock, this would imply a long distance migration of the YOY from offshore towards the Kongsfjorden ecosystem. It is unfortunate that there is to our knowledge no study in a similar area of the Arctic that focuses on the interactions and exchange between the fish communities of the shallow waters, deep waters, and pelagic realms.

However, it is generally known that fish of the same size classes spatially separate in different habitats. Especially, smaller fishes often prefer complex shallow water habitats to avoid predation and cannibalism as well as to use these habitats to access suitable food sources. That we did not catch specimen of *G. morhua* with a SL <10 cm in our nets could be explained by the theory that they gain a size of about 10 cm SL before migrating into the shallow water habitat of Kongsfjorden. Another explanation might be that we simply were not able to catch YOY specimen of *G. morhua* due to gear selectivity. The fyke nets and trammel nets we used had mesh sizes of 10 and 12 mm. The body height of *G. morhua* with standard length below 10 cm is expected to be smaller than 10 mm; therefore, they might have passed our nets without any detection.

Our study shows an increase in biodiversity along the south shore of the fjord from the west to the east. The water mass dynamics of Kongsfjorden may be the key to

Fig. 4 Multivariate analysis (MDS) of total catch per fish species per sampling site, based on square-root transformed data and Bray–Curtis dissimilarity index. Hierarchical cluster analysis was used to identify cluster with a similarity of >80 and >90 of 100



understanding this pattern in species distribution. Willis et al. (2006) showed the existence of a cyclonic and counter-clockwise gyre in the Kongsfjorden. Atlantic and Arctic water masses are mixed at the fjord mouth and are driven along the south shore to the inner parts of the fjord. Along the south shore, fresh water from the glaciers mixes continuously with the imported water masses. This results in a continuous reduction of salinity and a decrease in temperature, forming a gradient towards the inner parts of the fjord. Our study showed an increase of biodiversity and species evenness along this gradient from the westerly to the easterly sampling stations. *M. scorpius*, the most abundant and typically Atlantic species in this study, showed its highest abundance at the westernmost station Brandal, which is most influenced by Atlantic and, thereby, warmer and more saline water masses. The lowest CPUE for *M. scorpius* was found at the most eastern station Gåsebu. This station is most influenced by glacial melt water and, thereby, characterised by lower water temperatures and lower salinities. The reverse trend was found for *G. tricuspis*, a typical Arctic cottid fish species with anti-freezing proteins. Its highest abundance was found at the easternmost stations Gåsebu, its lowest abundances at the westernmost station Brandal. Low salinities and low water temperatures are characteristic for Arctic water masses. Thereby, this hydrographic gradient in Kongsfjorden resembles a small scale Atlantic–Arctic gradient. The reciprocal maximum in CPUE of *M. scorpius* and *G. tricuspis* along the south shore indicates a concurrency between the two species. This hypothesised co-occurrence between *M. scorpius* and *G. tricuspis* is most interesting with respect to the spatial distribution of fish along polar

gradients. *M. scorpius* is a generalist with respect to food sources with a fast reproductive cycle, and it can tolerate a wide range of salinities and temperatures (Ennis 1970; Luksenburg and Pedersen 2002). In contrast, *G. tricuspis* is a cold-adapted Arctic species with a smaller range of tolerated hydrography. It is possible that the two species are in competition regarding the same ecological resources such as food, and the differences in physiological adaption in combination with hydrography lead to this difference in small-scale geographical distribution. One factor could be the costs versus the advantages of the anti-freezing proteins of *G. tricuspis*. But it has to be noted that adaptive mechanisms to low temperatures and their metabolic costs are not yet universally accepted (Steffensen 2002). Moreover, the species-specific expression of cold adaptations with respect to seasonality and environmental parameters is still subject of research (di Prisco 2000; Enevoldsen et al. 2003).

On the shoreline of Blomstrandhalvøya, the sites Sørvågen and London that were constantly influenced by the water mass export from inner Kongsfjorden showed the highest abundance of *G. tricuspis*. Also they showed the closest resemblance to Gåsebu with respect to species abundance (Fig. 4). The sampling site Hansneset showed the most distinct pattern in species abundance and diversity that might be driven by its exposed position towards the mouth of the fjord, and a thereby diverse influence of different water masses at this site (Willis et al. 2006).

A further factor that influences the abundance and species diversity of the different sampling sites is the algal coverage. It is known that habitat structure is one of the most important factors for the temporal and spatial

distribution of fish abundance (Crowder and Cooper 1982; Johnson and Beaumier 1988; Persson and Eklöv 1995; Fischer 2000, 2004). In this study, we were able to show that the sites with highest species abundance with respect to CPUE were the sites with an algal coverage of 75–100 %, and the sites with the second highest coverage the one with 25–50 %. It can be assumed that the sites with the highest coverage and most structural complexity provided the best protection for fish, but also for prey. Sites with lower structural complexity represented therefore an easier feeding ground for fish, explaining the high CPUE at sites with 25–50 % algal cover. Only one site in this study (Brandal) showed an algal coverage of 50–75 %. The low CPUE at this class of algal coverage might thereby be an site-specific effect. Alternatively, it could be explained by the assumption that the intermediate algal coverage was not optimal for hunting and also not for structural protection. Therefore, it might have shown the least abundance of fish.

For sure, the assessment of this study can only be seen as a snapshot within a limited time scale and a limited number of sampling stations. Nevertheless, a more detailed future study about the influence of algae coverage on the Kongsfjorden shallow water ecosystem is advised. Future replications of this study should integrate a thorough habitat mapping and detailed hydrographic assessments to further analyse the link between fishes and habitat variables in Kongsfjorden. Further investigations on the importance of algal belts in Kongsfjorden as nursing grounds for fish are also warranted, and ongoing long-term observation by automatic camera systems like the Kongsfjorden Underwater Observatory (Fischer et al. 2016), could potentially improve our understanding of the year-round cycles of the fish and macrozoobenthos communities of Kongsfjorden. A publication about the inter-annual variability, assessed by automatic camera systems (Wehkamp and Fischer 2014) and fyke net fishing from 2012 to 2014 is currently in preparation. But also the replication of this study in shallow water systems of other Arctic fjords is necessary to understand if Kongsfjorden shows special characteristics or common trends. It is possible that the results of this study, especially, the dominance of boreal species are connected to changes in the algal belts and the macrozoobenthos community that have been documented by Bartsch et al. (2016) and Paar et al. (2016). To further explore the connection between the sampling sites and the fish community cooperative publications regarding growth rates, nutritional status, and trophic relationships of shallow water fishes at Hansneset are currently in preparation. In combination with future reassessments, this study can be used as a baseline for the detection of borealisation in Kongsfjorden.

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Compliance with ethical standards

Ethical approval All applicable international, national, and/or institutional guidelines for the care and use of animal were followed.

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